

BLASTN 2.2.12 [Aug-07-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1132600206-2671-153796666945.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
 3,579,719 sequences; 15,994,705,008 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

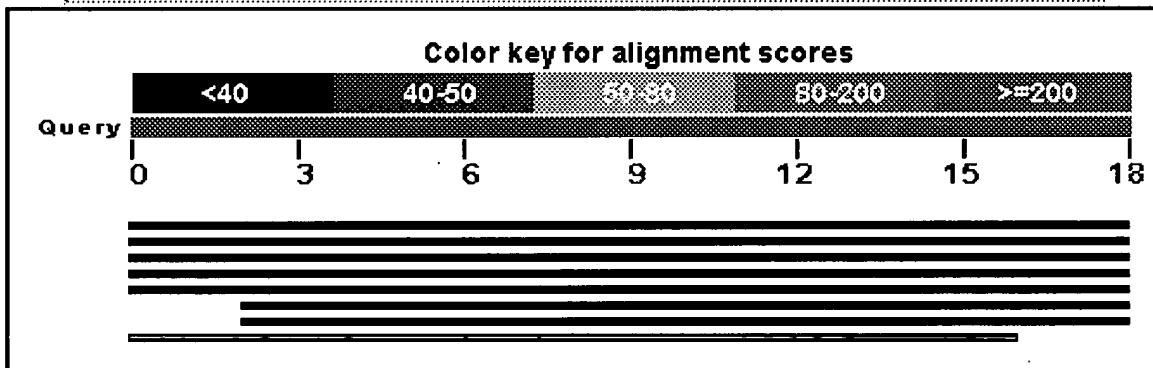
[Taxonomy reports](#)

Query=

(18 letters)

Distribution of 8 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Sequences producing significant alignments:	Score (Bits)	E Value
gi 33390917 qb AE017171.1 Staphylococcus aureus plasmid pLW043,	36.2	0.41
gi 21886737 qb AF516335.1 Enterococcus faecium plasmid pUW78...	36.2	0.41
gi 155036 qb M97297.1 TRNVAN Enterococcus faecium transposon ...	36.2	0.41
gi 43335 emb X56895.1 EFPVANAG E.faecium plasmid pIP816 vanA gen	36.2	0.41
gi 57790303 qb AY754011.1 Enterococcus faecium vancomycin re...	36.2	0.41
gi 12666232 emb AL161898.17 Human DNA sequence from clone RP...	32.2	6.4
gi 2370068 emb Z92540.1 HS179I15A Human DNA sequence from clo...	32.2	6.4
gi 479085 emb X79049.1 OTPDVANA2 O.turbata Plasmid DNA for vanco	32.2	6.4

Alignments**Get selected sequences****Select all****Deselect all**

> gi|33390917|gb|AE017171.1| Staphylococcus aureus plasmid pLW043, complete seq
Length=57889

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGTTT 18
|||||||||||||||||||
Sbjct 34773 CCGGTGGCAGCTACGTTT 34790

> gi|21886737|gb|AF516335.1| Enterococcus faecium plasmid pUW786 multiple antibiotic
gene cluster, complete sequence
Length=17510

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGTTT 18
|||||||||||||||||||
Sbjct 4222 CCGGTGGCAGCTACGTTT 4239

> gi|155036|gb|M97297.1|TRNVAN Enterococcus faecium transposon Tn1546 transposase
vanR (vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX),
vanY (vanY), and teicoplanin resistance protein (vanZ)
genes, complete cds
Length=10851

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGTTT 18
|||||||||||||||||||
Sbjct 7453 CCGGTGGCAGCTACGTTT 7470

> gi|43335|emb|X56895.1|EFPVANAG E.faecium plasmid pIP816 vanA gene for VANA ligase
Length=1768

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGTTT 18
|||||||||||||||||||
Sbjct 851 CCGGTGGCAGCTACGTTT 868

> gi|57790303|gb|AY754011.1| Enterococcus faecium vancomycin resistance protein A
partial cds
Length=614

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGTTT 18
|||||||||||||||||||
Sbjct 241 CCGGTGGCAGCTACGTTT 258

> gi|12666232|emb|AL161898.17| Human DNA sequence from clone RP11-270H22 on chr
sequence
Length=122839

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 GGTGGCAGCTACGTTT 18
|||||||||||||||
Sbjct 23455 GGTGGCAGCTACGTTT 23440

> gi|2370068|emb|Z92540.1|HS179I15A Human DNA sequence from clone RP1-179I15 on
a novel gene, a mitochondrial import receptor TOM22 pseudogene,
the 5' end of the KL gene for klotho, ESTs, STSs
and a CpG island, complete sequence
Length=146810

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 GGTGGCAGCTACGTTT 18
|||||||||||||||
Sbjct 115256 GGTGGCAGCTACGTTT 115241

> gi|479085|emb|X79049.1|OTPDVANA2 O.turbata Plasmid DNA for vancomycin resistance
Length=786

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGT 16
|||||||||||||||
Sbjct 345 CCGGTGGCAGCTACGT 360

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental

samples or phase 0, 1 or 2 HTGS sequences)
Posted date: Nov 20, 2005 2:03 AM
Number of letters in database: -1,185,164,172
Number of sequences in database: 3,579,719
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 3579719
Number of Hits to DB: 281356
Number of extensions: 8869
Number of successful extensions: 8869
Number of sequences better than 10: 2
Number of HSP's better than 10 without gapping: 2
Number of HSP's gapped: 8869
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10: 8867
Length of query: 18
Length of database: 15994705008
Length adjustment: 16
Effective length of query: 2
Effective length of database: 15937429504
Effective search space: 31874859008
Effective search space used: 31874859008
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 11 (22.3 bits)
S2: 16 (32.2 bits)